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#271632  
11/21/02

1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/435,471B

DATE: 11/21/2002

TIME: 09:50:04

Input Set : A:\USF-T135.ST25.txt

Output Set: N:\CRF4\11212002\I435471B.raw

3 <110> APPLICANT: Cooper, Denise R.  
 4 Patel, Niketa A.  
 6 <120> TITLE OF INVENTION: Glucose-Regulated mRNA Instability Element  
 8 <130> FILE REFERENCE: USF-T135  
 10 <140> CURRENT APPLICATION NUMBER: US 09/435,471B  
 11 <141> CURRENT FILING DATE: 1999-11-08  
 13 <160> NUMBER OF SEQ ID NOS: 13  
 15 <170> SOFTWARE: PatentIn version 3.1  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 7  
 19 <212> TYPE: PRT  
 20 <213> ORGANISM: Homo sapiens  
 22 <220> FEATURE:  
 23 <221> NAME/KEY: MISC\_FEATURE  
 24 <222> LOCATION: (1)..(7)  
 25 <223> OTHER INFORMATION: Tyrosine phosphatase conserved active-site motif  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: MISC\_FEATURE  
 30 <222> LOCATION: (2)..(6) ✓  
 31 <223> OTHER INFORMATION: Xaa = any amino acid residue  
 34 <400> SEQUENCE: 1

ENTERED

W--&gt; 36 Cys Xaa Xaa Xaa Xaa Xaa Arg

37 1 5  
 40 <210> SEQ ID NO: 2  
 41 <211> LENGTH: 11  
 42 <212> TYPE: PRT  
 43 <213> ORGANISM: Homo sapiens  
 45 <220> FEATURE:  
 46 <221> NAME/KEY: MISC\_FEATURE  
 47 <222> LOCATION: (1)..(11)  
 48 <223> OTHER INFORMATION: Tyrosine phosphatase signature sequence motif  
 51 <220> FEATURE:  
 52 <221> NAME/KEY: MISC\_FEATURE  
 53 <222> LOCATION: (1)..(1)  
 54 <223> OTHER INFORMATION: Xaa = Ile or Val  
 57 <220> FEATURE:  
 58 <221> NAME/KEY: MISC\_FEATURE  
 59 <222> LOCATION: (4)..(4)  
 60 <223> OTHER INFORMATION: Xaa = any amino acid residue  
 63 <220> FEATURE:  
 64 <221> NAME/KEY: MISC\_FEATURE  
 65 <222> LOCATION: (7)..(7)  
 66 <223> OTHER INFORMATION: Xaa = any amino acid residue

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69 <220> FEATURE:
70 <221> NAME/KEY: MISC_FEATURE
71 <222> LOCATION: (10)..(10)
72 <223> OTHER INFORMATION: Xaa = Ser or Thr
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78 1 5 10
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82 <211> LENGTH: 9
83 <212> TYPE: PRT
84 <213> ORGANISM: Homo sapiens
86 <220> FEATURE:
87 <221> NAME/KEY: MISC_FEATURE
88 <222> LOCATION: (1)..(9)
89 <223> OTHER INFORMATION: Dual-specificity phosphatase signature sequence motif
92 <220> FEATURE:
93 <221> NAME/KEY: MISC_FEATURE
94 <222> LOCATION: (3)..(4)
95 <223> OTHER INFORMATION: Xaa = any amino acid residue
98 <220> FEATURE:
99 <221> NAME/KEY: MISC_FEATURE
100 <222> LOCATION: (6)..(7)
101 <223> OTHER INFORMATION: Xaa = any amino acid residue
104 <220> FEATURE:
105 <221> NAME/KEY: MISC_FEATURE
106 <222> LOCATION: (9)..(9)
107 <223> OTHER INFORMATION: Xaa = Ser or Thr
110 <400> SEQUENCE: 3
W--> 112 His Cys Xaa Xaa Gly Xaa Xaa Arg Xaa
113 1 5
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117 <211> LENGTH: 33
118 <212> TYPE: DNA
119 <213> ORGANISM: Artificial Sequence
121 <220> FEATURE:
122 <223> OTHER INFORMATION: PKC-Beta-I and PKC-Beta-II upstream sense primer
124 <400> SEQUENCE: 4
125 cgtatatgcg gccgcgttgt gggcctgaag ggg 33
128 <210> SEQ ID NO: 5
129 <211> LENGTH: 33
130 <212> TYPE: DNA
131 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: PKC-Beta-I downstream antisense primer
136 <400> SEQUENCE: 5
137 gcattctagt cgacaagagt ttgtcagtgg gag 33
140 <210> SEQ ID NO: 6
141 <211> LENGTH: 21
142 <212> TYPE: DNA

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143 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:
146 <223> OTHER INFORMATION: Beta-globin sense primer
148 <400> SEQUENCE: 6
149 gcatctgtcc agtgaggaga a
152 <210> SEQ ID NO: 7
153 <211> LENGTH: 21
154 <212> TYPE: DNA
155 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION: Beta-globin antisense primer
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164 <210> SEQ ID NO: 8
165 <211> LENGTH: 351
166 <212> TYPE: DNA
167 <213> ORGANISM: Homo sapiens
169 <400> SEQUENCE: 8
170 ttttaaacca aaagcttttt gggcgaaacg ctgaaacttc gaccggtttt tcacccgcca
172 tccaccagtc ctaacacctc cgaccaggaa gtcatcagga atattgacca atcagaattc
174 gaaggatttc ctttggttaac tctgaatttt taaaaccgga agtcaagagc tagtagatct
176 gtagacctcc gtccttcatt tctgtcattc aagctcacag ctatcatgag agacaagcga
178 gacacctcca acttcgacaa aagttcacca ggcagcctgt ggaactgact ccactgaca
180 aactctgtcg actagaatgc cctgaattct gcagatatcc atcacactgc g
183 <210> SEQ ID NO: 9
184 <211> LENGTH: 39
185 <212> TYPE: DNA
186 <213> ORGANISM: Homo sapiens
188 <400> SEQUENCE: 9
189 taactctgaa tttttaaaac ccgaagtcaa gagctagta
192 <210> SEQ ID NO: 10
193 <211> LENGTH: 300
194 <212> TYPE: RNA
195 <213> ORGANISM: Homo sapiens
197 <400> SEQUENCE: 10
198 uuuuaaacca aaagcuuuuu gggcgaaacg cugaaacuuc gaccgguuuu ucacccgcca
200 uccaccaguc cuaacaccuc cgaccaggaa gucaucagga auauugacca aucagaauuc
202 gaaggauuuc cuuuguuaac ucugaauuuu uaaaaccgga agucaagagc uaguagaucu
204 guagaccucc guccuucuuu ucugucuuuc aagcucacag cuaucaugag agacaagcga
206 gacaccucca acuucgacaa aaguucacca ggcagccugu ggaacugacu cccacugaca
209 <210> SEQ ID NO: 11
210 <211> LENGTH: 175
211 <212> TYPE: RNA
212 <213> ORGANISM: Homo sapiens
214 <400> SEQUENCE: 11
215 uuuuaaacca aaagcuuuuu gggcgaaacg cugaaacuuc gaccgguuuu ucacccgcca
217 uccaccaguc cuaacaccuc cgaccaggaa gucaucagga auauugacca aucagaauuc
219 gaaggauuuc cuuuguuaac ucugaauuuu uaaaaccgga agucaagagc uagua
222 <210> SEQ ID NO: 12

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Input Set : A:\USF-T135.ST25.txt

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223 <211> LENGTH: 137
224 <212> TYPE: RNA
225 <213> ORGANISM: Homo sapiens
227 <400> SEQUENCE: 12
228 uuuuuuaccca aaagcuuuuu gggcgaaacg cugaaacuuc gaccgguuuu ucacccgccca      60
230 uccaccaguc cuaacaccuc cgaccaggaa gucaucagga auauugacca aucagaaauuc      120
232 gaaggauuuc cuuuguu                                     137
235 <210> SEQ ID NO: 13
236 <211> LENGTH: 25
237 <212> TYPE: PRT
238 <213> ORGANISM: Homo sapiens
240 <220> FEATURE:
241 <221> NAME/KEY: MISC_FEATURE
242 <222> LOCATION: (1)..(25)
243 <223> OTHER INFORMATION: Protein kinase ATP-binding motif
246 <220> FEATURE:
247 <221> NAME/KEY: MISC_FEATURE
248 <222> LOCATION: (1)..(1)
249 <223> OTHER INFORMATION: Xaa = any amino acid residue
252 <220> FEATURE:
253 <221> NAME/KEY: MISC_FEATURE
254 <222> LOCATION: (3)..(3)
255 <223> OTHER INFORMATION: Xaa = any amino acid residue
258 <220> FEATURE:
259 <221> NAME/KEY: MISC_FEATURE
260 <222> LOCATION: (5)..(6)
261 <223> OTHER INFORMATION: Xaa = any amino acid residue
264 <220> FEATURE:
265 <221> NAME/KEY: MISC_FEATURE
266 <222> LOCATION: (8)..(25)
267 <223> OTHER INFORMATION: Xaa = any amino acid residue
270 <400> SEQUENCE: 13
W--> 272 Xaa Gly Xaa Gly Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      273 1          5          10          15
W--> 276 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa
      277          20          25

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## RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 11/21/2002

PATENT APPLICATION: US/09/435,471B

TIME: 09:50:05

Input Set : A:\USF-T135.ST25.txt

Output Set: N:\CRF4\11212002\I435471B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2, 3, 4, 5, 6

Seq#:2; Xaa Pos. 1, 4, 7, 10

Seq#:3; Xaa Pos. 3, 4, 6, 7, 9

Seq#:13; Xaa Pos. 1, 3, 5, 6, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 25